

[illegible]

- 69 -

	150		155		180	
GCG ATG GTA	ATG GAT CGG CTA TAC	GGA GGT GTG TGC TAC	GCT GGG ATT		586	
Ala Met Val	Met Asp Arg Leu Tyr	Gly Gly Val Cys Tyr	Ala Gly Ile			
	165		175			
GAT ACC GAC	CCT GAG CTA AAA TAC	CCA AAA GGA GCT GGG	AGA GTT GCG		634	
Asp Thr Asp	Pro Glu Leu Lys Tyr	Pro Lys Gly Ala Gly	Arg Val Ala			
	180		190			
TTC TCT AAT	CAA CAG AGT TAC ATA GCT	GCT ATC AGT GCC	CGC TTT GTT		682	
Phe Ser Asn	Gln Gln Ser Tyr Ile Ala	Ala Ile Ser Ala	Arg Phe Val			
	195		210			
CAG CTG CAG	CAT GGA GAG ATA GAT AAA	CGG GTA AGC CTT	ATA CTA CAT		730	
Gln Leu Gln	His Gly Glu Ile Asp Lys	Arg Val Ser Leu	Ile Leu His			
	215		225			
TTT GGA AAA	TTC TAGAAATGGT CCTCTAAATG	TGTGATTACC AATATTAGAA			782	
Phe Gly Lys	Phe					
	230					
CGGGAGCATT	TTATGACAAT AAAGTGACAG	CTGACAATTT TGCCATAGA	GTAAATTATG		842	
GTCTATAATA	CATGAAATAA TGTCTATGA	ATTTCTTTTA TCITTCAGTT	TTTTGAGTAG		902	
CCTAATCAGA	ACACTACAAT TTACTTGAGT	TAATTTAATC TTCTCTAACT	TCCATTCAAT		962	
CTCAATCCAT	CGGTCCATTC ATTCACTTAG	TTTGTAAGTC ATTCAATAAA	TATTTACTGA		1022	
ATCCTTTTGT	CTGTGTTATA TCAAGTATAC	AAACAGGAAT GCCCTTGAGC	TTTCCTGCC		1082	
TTTTTTTGT	TGTGTTTTTA ATCCTGGGAC	ATAGGGAAGA CCTCAGCAAG	CCCTATTTCT		1142	
CAATGAATTG	TACTCACAGA TTTCCTTTT	TTTTTTTTTT TCITTTTCCA	CAGCCGOCAC		1202	
CTCTACCGA	TTTATCTCCT AGCTTGCTGT	TTCATGTATT CAACAAACGT	TTTAGTGCTT		1262	
AGGGCAAGAA	GTTCTGTGCC TCATGAGITT	ATTTCTAGC AGATAGAACT	GTATCACTTG		1322	
CCAGTACTAC	TCAGAGTGTG GCCTGTGGAC	TGACCTCCAG TCCTGAAACT	TAGTTGTAG		1382	
TGAGATAGGA	ATTTAGACCA GAATGTGTAA	TCAACCACAT TACTGGGCAC	AATGTTTGGT		1442	
CCAGCTGGCG	ATTTTTTTTT CATAGAAAAGC	CTTTATTGAT GAGGGAAGCA	ATATATTGAT		1502	
TTATATTTTG	GGGTACACCT TTATTTTCT	GGCACACTGG CACTTCATCT	CATGCTGACT		1562	
TGATATCCCA	TCACTCTGAG GCATTTGTCT	AAAAATAGATT GATTTTATCG	TGTTGTTCTC		1622	
AATTCAAGAT	GTAATAATCA TCAAGTCAGT	AGCAGTTTTT GCTTTTTATG	TTTCATGTCA		1682	
TGTACAGTCT	ACTTCACTGG CAGTAAAAAA	ATTTAAGATA GTGGTGGTCA	TCCTACAAAC		1742	
TGTGAATCTA	TTAAAGAGAA AAGTATCTGT	TCTATTCTAA GCATGGGGGA	GGGACAAGAT		1802	
TAGTATGTTA	ACATGCCTAC TTGTTTGT	TGAGATGGAG TCTCTCTCCG	TCACCCAGGC		1862	
TGGAGTGCA	TGGTACAGTC TCAGCTCAGT	CCAACCTCTG CTTCCCGGGT	TCAAGTGATT		1922	
CTCCTGCECT	AGCCTCCCGA GTAGGTGGAA	TACAGGCAT ATACCAAGAT	GCCCAACAAA		1982	
TGTTTGTATT	TTTAGTGGAG ACAGGGTTTC	ACCGTGTGGG TCAGGCCAGT	TTCAAACTCC		2042	
TGACCTCAAG	GGATCCACCT GCCTCACCCC	CTCAAAAGTG	TGGGATTACA	GGCATGAGCC	2102	
ACCCACCATG	CCTGGCCTAC TTGGTTTTTT	ATGCACACTA	AAAAATACCT	ACATCTCACT	2162	
GCCTTATTC	AACATAAGTT TCAGAGCTGT	GGGATTGGTC	ATTAGAAATT	CAGACTGAAT	2222	
TTGTGTTCT	CTGCAATGAA ATCCTTTGCC	CAGTGTTCAT	GTCACCTCTG	AGACATTATG	2282	
GAGCAGCCTA	GAGGCCAGAA GCCCAGTGCT	CTCCTTATGC	CTGCTCTTCG	TGGCGTTCTG	2342	
GACACTCTTC	TGTCCTTTTG GTACTTTTAT	TTTTTTAGTT	AAAAAATTTT	TTTTAGAGGG	2402	
AGGGTCTCAC	TCGTGTACCC AGGCTGGAGC	ACAGAAATCA	AATCATGACT	CAGTGCATGT	2462	

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TCTTCTCCTT	TGTTTCATGG	CTAATCTTGG	TCAGGATTCC	TTGTGAGAGC	TGGGTGGCAC	2522
CAGTGCTGGT	GACAGCCTGC	TGTAAGGGAG	TTTCAGCCAT	GAATCTCTCC	AGACTAAAAA	2582
TAACCAGCTC	TTTTCTAGCT	GATGAATTAA	TAACCAGGTG	ACTGTTAATG	CTTGAAAGGT	2642
TCACATGACA	GGTTGGCCGA	TAGAACGCTG	GAACAGGCC	AGTTTGTAGAA	ATTCACCTCT	2702
GACTTTTAGA	CTCAGGTGAA	CCATTCTTAC	TGAGAAAGAA	CAAAGCAGGG	TTTGTAGACTG	2762
TGAATCCTAT	GGCTGCATCT	TTTTTTTTTT	TTTAACAGAG	TTCCAGGTTT	GTGATTATAA	2822
CCCAACATGT	GTACACTATA	AATAGAAACC	ACGAGCCAGG	CTTTTTACGA	CAGCTCAGAA	2882
TCTTGTGACG	CAGTAGTCAG	GCATCTTCAC	ACCGACTTGA	ATATTGAAGT	GCAGTTGTGT	2942
GGAACCTTGA	TCATCTTAGT	TGATTTTGT	TAAATTATGA	TTCCACATAT	GACAAAAATC	3002
CAGATCCACT	AATTAAAATG	AGGGTTTATG	TCTATGAATA	ATCTCCTGTG	GGTTTAATCT	3062
CATAACATTG	TAGTCTAAAC	AGTTGGCTTC	ACTTCATGAT	GTCTGCTCAA	ATCCTTTTTT	3122
CTTTAAAGGA	TGTTTATTTA	ATAAGAAAAA	AAATGTAAAA	TGATAGATAA	TAAAGCCTT	3182
ACTAGGTCTT	TAAAGATGA	ACTATCCATA	TTTCAGTAAA	TGAATAATTA	GTCTTCCTC	3242
TTTGGGCACC	TTGGAACAGA	TTCATTGAGA	TAGTGGGTGG	AAATGTACAT	GTATGGTAAG	3302
CATTGCTGGC	CTAGTCACTG	AAAAATGTAA	ACTCTTATTT	TTGATTGCAG	GTGGAAGTTA	3362
AGCCATATGT	CTTGGATGAT	CAGCTGTGTG	ATGAATGTCA	GGGGGCCCGT	TGTGGGGGGA	3422
AATTGTGCTC	ATTTTCTGT	GCTAATGTTA	CCTGTCTGCA	GTATTACTGT	GAATATTGCT	3482
GGGTGCTAT	CCATTCTCGT	GCTGGCAGGG	AATTCCACAA	GCCCTGGTG	AAGGAAGGCG	3542
GTGACCGCCC	TCGGCATATT	TCATTCCGCT	GGAACATAAG	GATAACTGCA	GTGCTCATTT	3602
TCAGGCCTCA	GAATAAGTGC	ACTCTTCTGT	TCATTCTGAC	CCCTTCCTCA	ACCTCTTCAC	3662
GCTGGCATGT	CCTTTGTAG	CAGTCTGTAA	CTTAACATA	GTATAATGAA	AAGAATGACC	3722
TATAATATAG	GTGTTTGTGA	GATTCTTGTG	TCACTGCAAA	CAATATGAAC	TCCTTTTTCG	3782
TATTGCCATC	GGGTGTCATG	GAAGTTTAT	TCTCTTGT	TGCTGGAAC	CAAGAGGATC	3842
CAAACCTCCT	GCAACATTTT	CTTAGAGGAG	AGAGAGAAAT	ATTAAAAGAG	AAATGAAACA	3902
ATAGAGTATT	TTGGGTTTTT	AATTAAATTA	TTGTTAATAA	TATAACATAT	AAGAATACIT	3962
TTATTAAAAA	AACCATGCAA	CAATAACACT	ATCGGTCTAT	CTGACAGTTT	TTCCCCCAGG	4022
GAAGTGCTTT	TGCCTTTTCC	TTTCTTTTTT	TTTTTTTTTT	ATCTTTTTTG	TTCTCTCTCT	4082
TTTTTCCATC	CCTTTTAAAT	TTTTTTAAACA	GCAATGGAGG	AAGTTAACAA	TTTTTAATGG	4142
AAAGAGCATG	TTAGAGCAAA	CAATGCATA	AGCAAGACTG	AGCAGCATT	TAATTAATTT	4202
TCAGGGTTTT	GAGGCTGAAC	ATAATTTTCAT	TATCCCTCAA	AAAGTTACCA	CCACATCAGA	4262
AAAAAAAAAA	AAAA					4276

SEQ ID NO:2

SEQUENCE LENGTH: 2689

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:2

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AAAAATTTGAA	CCTTTTGGAG	CTGTGTGCTA	AATCTTCAGT	GGGACA	ATG GGT TCA	115

															Met Gly Ser	
															1	
GAC	AAA	AGA	GTG	AGT	AGA	ACA	GAG	CGT	AGT	GGA	AGA	TAC	GGT	TCC	ATC	163
Asp	Lys	Arg	Val	Ser	Arg	Thr	Glu	Arg	Ser	Gly	Arg	Tyr	Gly	Ser	Ile	
5			10			15										
ATA	GAC	AGG	GAT	GAC	CGT	GAT	GAG	CGT	GAA	TCC	CGA	AGC	AGG	CGG	AGG	211
Ile	Asp	Arg	Asp	Asp	Arg	Asp	Glu	Arg	Glu	Ser	Arg	Ser	Arg	Arg	Arg	
20			25			30			35							
GAC	TCA	GAT	TAC	AAA	AGA	TCT	AGT	GAT	GAT	CGG	AGG	GGT	GAT	AGA	TAT	259
Asp	Ser	Asp	Tyr	Lys	Arg	Ser	Ser	Asp	Asp	Arg	Arg	Gly	Asp	Arg	Tyr	
40				45				50								
GAT	GAC	TAC	CGA	GAC	TAT	GAC	AGT	CCA	GAG	AGA	GAG	CGT	GAA	AGA	AGG	307
Asp	Asp	Tyr	Arg	Asp	Tyr	Asp	Ser	Pro	Glu	Arg	Glu	Arg	Glu	Arg	Arg	
55			60			65										
AAC	AGT	GAC	CGA	TCC	GAA	GAT	GGC	TAC	CAT	TCA	GAT	GGT	GAC	TAT	GGT	355
Asn	Ser	Asp	Arg	Ser	Glu	Asp	Gly	Tyr	His	Ser	Asp	Gly	Asp	Tyr	Gly	
70			75			80										
GAG	CAC	GAC	TAT	AGG	CAT	GAC	ATC	AGT	GAC	GAG	AGG	GAG	AGC	AAG	ACC	403
Glu	His	Asp	Tyr	Arg	His	Asp	Ile	Ser	Asp	Glu	Arg	Glu	Ser	Lys	Thr	
85			90			95										
ATC	ATG	CTG	CGC	GGC	CTT	CCC	ATC	ACC	ATC	ACA	GAG	AGC	GAT	ATT	CGA	451
Ile	Met	Leu	Arg	Gly	Leu	Pro	Ile	Thr	Ile	Thr	Glu	Ser	Asp	Ile	Arg	
100			105			110			115							
GAA	ATG	ATG	GAG	TCC	TTC	GAA	GGC	CCT	CAG	CCT	CGC	GAT	GTG	AGG	CTG	499
Glu	Met	Met	Glu	Ser	Phe	Glu	Gly	Pro	Gln	Pro	Ala	Asp	Val	Arg	Leu	
120				125				130								
ATG	AAG	AGG	AAA	ACA	GGT	GAG	AGC	TTG	CTT	AGT	TCC	TGATATTATT	545			
Met	Lys	Arg	Lys	Thr	Gly	Glu	Ser	Leu	Leu	Ser	Ser					
135			140													
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GCACATGAAT	TCAGAATGAA	AGGTTTGCCA	TGGCTAAGGA	ATGTGACTCT	TTGAAAACCA	665										
TGTTAGCATC	TGAGGAACCT	TTTTAAACTT	TGTTTTAGGG	ACTTTTTTTT	CCTTAGGTAA	725										
GTAATGATTT	ATAAACTCCT	TJTJTJTJT	TTGACTATAG	TCGGTTGCAT	GGTTACTTTA	785										
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TATCAAGAAG	ATCCCCAAGT	CAAGTCACAT	TTGTAAGGCT	GCTTCCCAAT	TGGCTTTGTC	905										
ACGCAGTGT	GAAGCAGTGG	GAGCAGAGAT	CAACTGTTAT	AAAGGAACATG	ACTAACACAA	965										
GTATCCCGCT	TATATCTGAA	TGCTGTCTCT	AGGTGTAAGC	CGTGTTTCG	CCTTCGTGGA	1025										
GTTTTATCAC	TTGCAAGATG	CTACCAGCTG	GATGGAAGCC	AATCAGGTTG	CTTCACTCAC	1085										
CAAGTCTAGA	TATTCATGAA	AATGGAACAA	GTCTGTACAA	TTTTAAAAAA	AGGTTGAAGG	1145										
AGTGGTTTGT	TCCAAAGGAG	TGACTTTTTT	TTAAAAAAA	AAGCTTTGTA	TATATTAAAA	1205										
TTGATGTTAC	TAGAATAAGT	ACAGTACCAA	GGACTTCATT	ATAGAATTTG	TTCTGCCTTT	1265										
AAACATGGCT	ACCTACCTGG	CAGGGCTTTG	TTAAGTACTG	AATACCTGTG	TGGTAATCAC	1325										
TAAAAACATCT	TAATGTTTCT	CCTTTTCTTA	GTTTGTTATA	TTCTTATTAT	TGCCATTGAG	1385										
AGTAAGCTTA	GATATCAAAA	CTCTCCATTA	GACAGTGAAG	AGAACATAGT	GAAAGTCTGT	1445										

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CGTAACGCT CAGACCGGC TTCAGGGAAT ATTTAAGGAC TTAGTGAAT TTATGAACAA 1565
TAAGTCTGAT GAGATTAGCC TGGGAGTGGT GTCCTGCAGC TGTCTAATCT AGTTAGAGTG 1625
GCATTAACT TCTAATCTCC TTGAGAAATG CTTTATAGT CTGTTCAAAG CAAGTCATTG 1685
ATGGTTCTTC GAGGTAGTGT TAACTGAAGT GTTCTTCAGT TTGTCAAGAT AATGTTCACT 1745
GCTTGGCACT TAAATAACAT TTTTGGCAAG AACTCCAAGG CACATTATTG AATGCCTTTA 1805
ACCAAGTGCA TTCTGGGAAG TTTGCTTGAC TCATTATCTT GCTTTTCTGC AGCATTCTGT 1865
GATTTGAGTC ATCCATGAAT CCATGAATAA AAGTTACATT CTTTGATTGG TAATATTGCC 1925
ATTTATAACA AGACTCACTA ATGAGGGTAT CACTTTGACT GACTGATTGG TTAAAGTTTT 1985
TAAGCCTCTC ATTTTCCTAA CCCAGAAATC ACAGCCTGAT TTTATTAATA GTAGAGCTTC 2045
ATTCAATTCA TACCATAGAT ACCATCCTAG TAAATCCAGA ACATATACAA GGTTCAATGTG 2105
AGTCTGCTTT CTTGACATGA TAGCATTGTT TGATGCAGTG GATATGTCAG AATGACTAAC 2165
CTAGGAGTTT AAAACTCCTA AGAAACTAAA ACCTGTAAGA CATTTAAAG TCTCCACAAT 2225
TTTAATGTAT ACAAAGCTAT GTTACTGTGT AACACATTAC AGTTCAAAT CACTCCAGAA 2285
ATAAAAGGCC AGTAGGATTA GGGACTCACT GGTAGTTTGG AGTCTCCAG CACACATGCC 2345
TCCTAGTGGG ATGATCTATT CACATATCTC CCAGCTTTTT TATTTTGGCT TCTGTATATC 2405
ACAGTGAGTG GATGGCCCTT CAGCTTTTTC TCTCTGGCC AGACATGCAG TCTTGCCTTT 2465
AGATATCGCA GAGACAAAAT TCACAGCATG TCTTAAATCT TCCAGGATT GCAAGAACCA 2525
AATTGCTCAA CAGTATGTAT GTTTAGAGGG GTTAGACTCC TTTTAAAAAT CTGGATATCT 2585
AACCACCTAC TTAATCTGT TTGATAGTGT CAAACCACCC CCACCTTGA TCCTCCACC 2645
CCCAAAAAA AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAA 2689

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SEQ ID NO:3  
 SEQUENCE LENGTH: 2981  
 SEQUENCE TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE  
 ORGANISM: human  
 CELL TYPE: leukocyte  
 SEQUENCE DESCRIPTION: SEQ ID NO:3

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GCTGGGACAA CAGGCACCTG CCACCAGGCC GGGCTAATTT TTTGTATTTT TAGTAGAGAC 180
AGGGTTTCAC CATGTTAGCC AGGATGGTCT CAATCTCCTG ACCTCGTGAT CCACCGCCT 240
CAGCCTCCCA AAGTGCTGAG ATTACAGGTG TGAGCCACCA CGCCAGCCA CATCTTCTT 300
TCTTTCTTTT TGGTTTTTGT TTGTTGTTG AGACAGGGTC TTGCTCTGTC GCCCTGGCTC 360
ACGTGAACCT CCCACCTCAG CCTCCCAAGT AGCTGAGACC ACAGGTGTGA GCCACCACTC 420
CTGGGTAATG TTTGTATTTT TTTGTAGAGA TGGGGTTTCA CCGTGCTGCC CAGACTGCTC 480
TCAAACCTCT GGGCTCAAGT GATCCACCTG CCTTGACCTC CTAAAGTGCT GGAATTACAG 540
GTGTGAGCCA CCGTGCTCAG CCGAGTGCTT TTCGTATGTT TTCTGAGCAC GTGGATTTC 600
ATCTCTCTGC ATTCTCTGTT CATCTCAGCC TGTTTGTTC ATTGAGATAA ATGACTTTT 660
CTTGGTAACCT TAGAGTACTT TGTGTATTTA CAGGTTAATC CCTTATCAAT TTATATCAGT 720

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TGCTGCTATC TTTTCTTAGA TTTTCTTTT CATTTTAAAA ATTACATTGT TTCAATGAAC	780
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AGGGTCTTGT TTAAGAAATC GTTCTTTATC CTGAGGTCAT AAAGATAGTC TACTGTATTT	900
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TGGGGATAAG GATCACAATT TTATTTTATT TTTTTCAC TTGGTTATGC CAGTGGCCCC	1020
ATTTCCATTT TTTGAATAGT CTTTCTGTGC AGAAAAGACT TCACTAGCAG AGAAGTCTCG	1080
AGACTTACCC TTCAAAAGGC CCCATTACAC AGGCTAGCAC TTGGCGTGCA TCTGAGAACC	1140
TGGATTTTGG GGTGGTTCCT ATAATGTGGT GTATGCTGAA CACCCACCTT TCCTTCTGGG	1200
AGTCTGGAAT TTGGGTATAT GTTGGACAGA GGCTGCCTAA GTGACCAGCT TCAACAACAG	1260
CCCTGGGTGC TGGGTCACTC ATGACCCATA GACAAA ATG CCA CAC ATG TTG TCA	1314
Met Pro His Met Leu Ser	
1 5	
CAG CTT ATT GCT GGA GGA GTT AGC ACA TCC TGT GTG ACT GCA CTG GGA	1362
Gln Leu Ile Ala Gly Gly Val Ser Thr Ser Cys Val Thr Ala Leu Gly	
10 15 20	
GAG GAA ACT GGT GCC TGG TTC CCT GTG TAT TTG TCC CAC GCC TCC AGT	1410
Glu Glu Thr Gly Ala Trp Phe Pro Val Tyr Leu Ser His Ala Ser Ser	
25 30 35	
CCC TTT GCT GAT CTC GTT TTT TGT CCT TTT GCT GAG ATA AAT CAC AGC	1458
Pro Phe Ala Asp Leu Val Phe Cys Pro Phe Ala Glu Ile Asn His Ser	
40 45 50	
CAG GAG TAT GAC AAT ATG CGG GGT CCT GTG AGT CCT CCT AAC AAA CAG	1506
Gln Glu Tyr Asp Asn Met Arg Gly Pro Val Ser Pro Pro Asn Lys Gln	
55 60 65 70	
TTC AAT CTG GGG GTG ATC TTT GGG ATC CCC AAC AAC TGT CGT TTC CCC	1554
Phe Asn Leu Gly Val Ile Phe Gly Ile Pro Asn Asn Cys Arg Phe Pro	
75 80 85	
ACT GAT AAT AAA ATA ACT GAG AAG CAG CTA TTG GGC AAT GTT CTG AAC	1602
Thr Asp Asn Lys Ile Thr Glu Lys Gln Leu Leu Gly Asn Val Leu Asn	
90 95 100	
TAC CCT TGAACATTCA TGTCTTCATC TGAACATCCA TCTACTACCC CTGATTTTTT	1658
Tyr Pro	
104	
CAGTGCAGGG TGCATATCCT GTATCACCCA ATAAATGGTC ATTGATCACC ATAGGAAAGG	1718
AACAGTGAAG GCTCCACGGT GGTTTGGAGG AAGGTGGCAG GCATTACGCG GTAACTTTTT	1778
TGAGCAGATA GATTTTATGT TTTTGCAATG AGTGAAATAA ATTTTCCCAT ATCTATTTAA	1838
GGTTGGCAAT CATTATCTTT TTATCATCTT GGAACATTTG GAATTCCTTT AATATGTTTA	1898
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CGGGCTCCTC ATACCTGCCT GTGTGATTTC TAACATGTCA CGCTATGCAA CCAGTTGCTT	2018
TACTTTGTAG AGTGTTCCTT TAGGTAATAG CTTATTATTG GTTATGTGAT TACAGTGTGT	2078
TAAAGACAGG TCTGTAGTTA TGTAAATGC CGTTTCTCTG AGTATCATGG TCATTTCAC	2138
ATATTTCTCT ATTCATGTAT TTGTAAGAAT ATATCTATTT TTGCAGTATT TTATTTATTT	2198
ATTTTATTTT ATTTTCTGAA ACGGAGCCTT GTTCTGTAC CTAGGCTGGA GTGCAGTGGT	2258
GTGATCTCGA CTCACGTGA CCTCCCCCTC CCAGGTTCAA GCGATTCTCC CGCCTCATCC	2318



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70	75	80	85	
TTG GAG TTG ATG CTG CAT TTT TAT TCT GTG TTA AGT CTT GAA CCT GCT				584
Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu Ser Leu Glu Pro Ala				
	90	95	100	
GTT GCT GAA CAT TGG TCA GGG GAA TTT GAG AAG TGG AAA GTG GGC TTT				632
Val Ala Glu His Trp Ser Gly Glu Phe Glu Lys Trp Lys Val Gly Phe				
	105	110	115	
TTT CAC CCT TTG AAA AGA GAG GAT GGA TTC TTC ACC AGA ACT GAC ATT				680
Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe Thr Arg Thr Asp Ile				
	120	125	130	
TAAAAAAGT CAGCGTGGCA CGTTTATGTA TGTGTGGCAG ATCTAAASAG ACAATATTTT				740
GATCTCAGGA GTGTTTATTC TTGAACCATC TTCAGAACTC TAAGATTTGA GAAATAATAA				800
AATATTGACC ATCCTTCAAA GAGAAAAACA CAGGGCGATC TTTGGCATAG CCTGTCATTT				860
TGCTCACATT TCACTTCTCT CTCTCCAAC TCAAGAGCCCC TGCTGTGGAA CAGGTGCTGT				920
GCTGGGTGGC AGGGGAGGTC TCTGGCTTTT TTTTITTTTG ATCTCGTCT TAACATCTAG				980
CCTACTGGAG GAAGTGTATT TAATCATCCA CTTATCTGTT AACAATTATC TCTGAGGGCC				1040
CGTCACATTC AGAGAAGATT CTAGGTTCCT TACAAGTATC CTCTCACTGT GTACATACTA				1100
AATCAACATC CTGCTGGATT TCCCCAGAC ATCTCCCTTC ATCACCATTG GAGAGTATCC				1160
TCTAATTGCC AGCCCTATTC ACCATACTCA TCTCATTTGA TCTGGAGTTT TCTGAGAGTG				1220
ACCGGGGGTG GGATGGACAG GATAATTTAG CAAGAGTGTA TAAGTAAAT CTATATAATA				1280
AAAGTTATCT CCTGTGCCC CCCATGATCT ATCTTTATG TAGCAGTCTG AATGAGATTT				1340
TCAGAAACAA GAACCACTTT ACCTTAGTCT CTCTCTCTTC TTCTTCTCT TTTCTTTTCT				1400
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A				1461

SEQ ID NO:5

SEQUENCE LENGTH: 3329

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:5

CCAAAGTGCT GGGATTATAG GCATGAGCCA CTGCGCCCGG CCAGAATACC CTATCCTTAA	60
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TTGGCAGAGG CCTGTGGCCT CCAGTATTTT GAGGGAGCTG AGGGCCACTG ATCTCTCCAT	180
ATGCTCTCAA CATCATGGGA CTAGTAGGAT GAAAGCAAGC CTCAGACCAG ATTCTACCTC	240
AAGCAGGCAC ACAACATTC ATGCAGCTTC TACTTGGAGC CTGATGAAGT TCAAATTGTT	300
TGTCCTCTGA GGCTCTCTTT GCATGGAAAT TTCTCCCATG ACAGATGAGA AAGTTCTGGG	360
GCAGCATTCA GCTTCTAGT TGGATTAGGC AACAGAATCC TTTGAAAATG TCTGTGCACA	420
GACCAGGTGG CTCTCTGGGC CAGTGTACTC TGAAGATGT GTGTCTGGC CTAGCTGGTT	480
GAGGAAAAGC AGGGCAAGCC TAGCCAAATC ACACATCTTG AACAGCCCTC ATTCGTTATA	540



CTAACTTTCC CACCCTCGG TGTGTATAGG AGATAAAGAT GGCAGACGTG CTATTAGGCT	600
GCCAATGGGA GTGGGCTCTG ATATGGTCTT TCAAAT ATG AAT CAC CCC TGG CAT	654
Met Asn His Pro Trp His	
1 5	
GTG TGT TTC CTG TTT AAG GTT CTC AGG TAT TAC CCA ACT GCA CCA ATA	702
Val Cys Phe Leu Phe Lys Val Leu Arg Tyr Tyr Pro Thr Ala Pro Ile	
10 15 20	
TTA AAA TGG ACA CAT ACC GTG TCA TGC AGT TGG TGC CGA AGT GTT TTA	750
Leu Lys Trp Thr His Thr Val Ser Cys Ser Trp Cys Arg Ser Val Leu	
25 30 35	
AGG GAA GTT GTA GGC AAT GTG AGT TTA TCA GAA AAC TTC ACC ATA TCA	798
Arg Glu Val Val Gly Asn Val Ser Leu Ser Glu Asn Phe Thr Ile Ser	
40 45 50	
GCA TTT TGC CCT GAG CTT ACA CCA TTC CCA GAT CAA GGT ACA AGC ACA	846
Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro Asp Gln Gly Thr Ser Thr	
55 60 65 70	
ATG ATT TCC TTT CTT GAA AAG TTC AAC AAA AGC AAG AGA GAG AGA TTG	894
Met Ile Ser Phe Leu Glu Lys Phe Asn Lys Ser Lys Arg Glu Arg Leu	
75 80 85	
GAG TTG ATG CTG CAT TTT TAT TCT GTG TTA AGT CTT GAA CCT GCT TTT	942
Glu Leu Met Leu His Phe Tyr Ser Val Leu Ser Leu Glu Pro Ala Phe	
90 95 100	
GCT GAA CAT TGG TCA GGG GAA TTT GAG AAG TGG AAA GTG GGC TTT TTT	990
Ala Glu His Trp Ser Gly Glu Phe Glu Lys Trp Lys Val Gly Phe Phe	
105 110 115	
CAC CCT TTG AAA AGA GAG GAT GGA TTC TTC ACC AGA ACT GAC ATT TAAAAA	1041
His Pro Leu Lys Arg Glu Asp Gly Phe Phe Thr Arg Thr Asp Ile	
120 125 130	
AAGTCAGCGT GGCACGTTTT AGTATGTGTG GCAGATCTAA AGAGACAATA TTTTGATCTC	1101
AGGAGTGTTT ATTCTTGAAG CATTTTCAGA ACTCTAAGAT TTGAGAAATA ATAAATATT	1161
GACCATCCTT CAAAGAGAAA AACACAGGGC GATCTTTGGC ATAGCGCTCTC ATTTTGCTCA	1221
CATTTCACCT CTCTCTCTCC AACTTCAGAG CCCCTGCTGT GGAACAGGTG CTGTGCTGGG	1281
TGGCAGGGGA GGTCTCTGGC TTTTTTTTTT TGATCTCCGT CTTAACATCT AGCCTACTGG	1341
AGGAAGTGT ATTAATCATC CACTTATCTG TTAACAATA TCTCTGAGGG CCCGTACAT	1401
TCAGAGAAGA TTCTAGGTTT TCTACAAGTA TCCTCTCACT GTGTACATAC TAAATCAACA	1461
TCCTGCTGGA TTTCCTCCAG ACATCTCCCT TCATCACCAT TGGAGAGTAT GCTCTAATTG	1521
CCAGCCCTAT TCACCATACT CATCTCATTT GATCTGGAGT TTCTTGAGAG TCACCGGGGG	1581
TGGGATGGAC AGGATAATTT AGCAAGAGTG TATAAGTAAA ATCTATATAA TAAAAGTTAT	1641
CTCCCTGTGC CCCCCTATGAT CTATTCTTTA TGTAGCAGTC TGAATGAGAT TTTCAGAAAC	1701
AAGAACCACT TTACCTTAGT CTCTCTCTCT TCTCTCTCT CTTTCTTTT CTITTTTTTT	1761
AGTATTATGG GGATCTGTTT CTGTGGCCCA GGGTGGAGTG CAGTGGTATG ATCTTGGGCTC	1821
ACAGCAGCCT TGAAGTCCCG GGCTCAAGTG GTCTCTCTGG TCTGCTCTCC CTAGTAGCTA	1881
GGACCTGACGG TTGTGTCGAC CACACCTGGC TAAATGAAAA AAGAAATTTT TTTCCAATAG	1941
ACAGCAGTGT TTGCTATGTC CCCAGGCTGG TCTCAAACTC CTGGCCTCAA GTGATCTCTC	2001





00000572.030499

TTTAAATTAT ATGGCTTGAG TTAAATTGT AATAGGCGTA ACTAATTTTA ACTCTATAAT 2116  
GTGTTTCATTG TGAATAATC CTAAACATAT GAATTATGTT TGCATGTTCA CTCCAAGAG 2176  
CCTTTTTTTG AAAAAAAGCT TTTTITGAAT CATCAAGTCT TTCACATTTA AATAAAGTGT 2236  
TTGAAAGCTT TATTTAAAAA AAAAAAAAAA AAAAAAAAAA 2276

SEQ ID NO:7

SEQUENCE LENGTH: 165

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:7

CACTTATAAA ATGTTAGGGC TTAATATTAT TCATAGATCG AGGATAGTTT CATTCTTAGT 60  
CGCCTCCTTA GTCACCTCTC CTATACCAAT CTGAGACCAT TTTACAATTT AGAAAAGACA 120  
AATAACTGGT TGGTTACTT GATAGTATAA TAACC 155

SEQ ID NO:8

SEQUENCE LENGTH: 278

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:8

GAAGGAGAAT ATGAAGAGGT TAGAAAAGNT CNGGNTTCTG TTGGTGAAAT GAAGGATGAA 60  
GGGGAAGAGA CATTAAATTA TCCTGATACT ACCATTGACT TGTCTCACCT TCAACCCCAA 120  
AGGTCCATCC AGAAATTGGC TTCAAAGAG GAATCTTCTA ATTCTAGTGA CAGTAAATCA 180  
CAGAGCCGGA GACATTTGTC AGCCAAGGAA AGAAGGGAAA TGAAAAAGAA AAAACTTCCA 240  
AGTGACTCAG GAGATTTAGA AGCGTTAGAG GGAAAGGA 278

SEQ ID NO:9

SEQUENCE LENGTH: 135

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

00000672.050490

SEQUENCE DESCRIPTION: SEQ ID NO:9  
TTCTGACAAT GAGTAAGAAG AAAGAGGGTC TTGCCCTTGT GTTATTAAGA TTTATCATAG 60  
AGCAATAATA ASTAAATCGG TGTATACCA GCACAGAGAT TAGACAAATA AACCAAGGGA 120  
CTGGACTAAA TAAGC 135

SEQ ID NO:10  
SEQUENCE LENGTH: 197  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:10  
ATGGTACCCA GTTTCAAATT AACATGGTTA TTTTACTTGT GTTCCCAAAT TTAACATTAG 60  
GGAATTTTGT GTTGTGGGTC TGTATCACT AGAAAAATAT ATATATTGGT GCTGAAGATA 120  
ATTTTGAGAT AATTAGACAA GACAGTTTAG CATTTACAAG AACAAAGTTTG GCAGTTGAAG 180  
AATCTATTTA TATGACT 197

SEQ ID NO:11  
SEQUENCE LENGTH: 137  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:11  
CCACCGCACC TGGCTGATGC TTTTCTATCT GACTTCTTTC AGAGGACCTT GAAAGACACT 60  
AAGTGGAAATC TTTCCTTGAA GTCCTCCAAG CTAACAACAAT TCTCTGGAAA GATCACCTCT 120  
GTTCACTCCT GGTCTCT 137

SEQ ID NO:12  
SEQUENCE LENGTH: 274  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:12



564630-2250060

TATAAGGWG GAACCTTACT ATCTTAATG ACCTTACTGA TGCTGACTTT AATACTCTGT 60  
GAAGGTTAGA GTTCAGTGAA TGTTACCTAG AACAGCCCC GGCTGTGGAA TACTTTATTC 120  
TTAGCCCTAT ATTTGGGGTT TGGATGTCCA CTGTGCTGGT TCCCAGAGAT AGTAAGGGGA 180  
TGAGAGTATT GGTACATCT CCTGACCCAC ATACTTAAGA TCCAGATGAA CAAGACAGTT 240  
TTCACCTCTG CTGGTAGAA CCTATTTGK SHAGGAAACA GYTCTAAAG AATGGTTCTA 300  
GCCAGACCT GTCGYTACCA GAA 323

SEQ ID NO:16  
SEQUENCE LENGTH: 138  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:16  
AGTATGACAA ATAGTTTCTG CCTGATTGGT GAGATTGGG ATGGGCCCC ACTTTGTTTC 60  
TCCTTCTGCA TAAAAATTTC AACATTTTCA CAAAATTTTC AAAAATCTCT CCTCAGTCTG 120  
TACATCTTTG TTAATCAG 138

SEQ ID NO:17  
SEQUENCE LENGTH: 135  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte  
SEQUENCE DESCRIPTION: SEQ ID NO:17  
TGATCCCCAC AATTCTTGT GATTGGTGAG GAACTATAAA TGAATCCAT CCAAGCTTAT 60  
ACCAGAAAAA AGGAGCAGAT TTCTACAAA TTATATCATT TTTAATCCAT TACCACATTA 120  
TTTTAGGGGA ACTAC 135

SEQ ID NO:18  
SEQUENCE LENGTH: 219  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte





$$\begin{array}{ccccccc} \frac{\partial^2 u}{\partial x^2} & = & -\frac{1}{2} \frac{\partial^2 v}{\partial x^2} & + & \frac{1}{2} \frac{\partial^2 w}{\partial x^2} & + & \frac{1}{2} \frac{\partial^2 z}{\partial x^2} \\ \frac{\partial^2 u}{\partial y^2} & = & -\frac{1}{2} \frac{\partial^2 v}{\partial y^2} & + & \frac{1}{2} \frac{\partial^2 w}{\partial y^2} & + & \frac{1}{2} \frac{\partial^2 z}{\partial y^2} \\ \frac{\partial^2 u}{\partial z^2} & = & -\frac{1}{2} \frac{\partial^2 v}{\partial z^2} & + & \frac{1}{2} \frac{\partial^2 w}{\partial z^2} & + & \frac{1}{2} \frac{\partial^2 z}{\partial z^2} \\ \frac{\partial^2 u}{\partial t^2} & = & -\frac{1}{2} \frac{\partial^2 v}{\partial t^2} & + & \frac{1}{2} \frac{\partial^2 w}{\partial t^2} & + & \frac{1}{2} \frac{\partial^2 z}{\partial t^2} \end{array}$$

SEQ ID NO:24  
SEQUENCE LENGTH: 251  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double

[illegible][illegible][illegible][illegible]



Figure 1 displays a series of chemical structures, labeled (a) through (l), representing various substituted benzene rings and their derivatives. The structures are arranged vertically and include various functional groups and substituents.

Figure 1 displays a series of chemical structures, labeled (a) through (l), representing various substituted benzene rings and their derivatives. The structures are arranged vertically and include various functional groups and substituents.

Figure 1 displays a series of chemical structures, labeled (a) through (l), representing various substituted benzene rings and their derivatives. The structures are arranged vertically and include various functional groups and substituents.

ACAAATATTTA CTGCAAAAG AGCCACACAGA GACATGTCAA TGAAGTCATA G

291

SEQ ID NO:33

SEQUENCE LENGTH: 230

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:33

Met Glu Asp Gly Phe Leu Asp Asp Gly Arg Gly Asp Gln Pro Leu His  
1 5 10 15  
Ser Gly Leu Gly Ser Pro His Cys Phe Ser His Gln Asn Gly Glu Arg  
20 25 30  
Val Glu Arg Tyr Ser Arg Lys Val Phe Val Gly Gly Leu Pro Pro Asp  
35 40 45  
Ile Asp Glu Asp Glu Ile Thr Ala Ser Phe Arg Arg Phe Gly Pro Leu  
50 55 60  
Ile Val Asp Trp Pro His Lys Ala Glu Ser Lys Ser Tyr Phe Pro Pro  
65 70 75 80  
Lys Gly Tyr Ala Phe Leu Leu Phe Gln Asp Glu Ser Ser Val Gln Ala  
85 90 95  
Leu Ile Asp Ala Cys Ile Glu Glu Asp Gly Lys Leu Tyr Leu Cys Val  
100 105 110  
Ser Ser Pro Thr Ile Lys Asp Lys Pro Val Gln Ile Arg Pro Trp Asn  
115 120 125  
Leu Ser Asp Ser Asp Phe Val Met Asp Gly Ser Gln Pro Leu Asp Pro  
130 135 140  
Arg Lys Thr Ile Phe Val Gly Gly Val Pro Arg Pro Leu Arg Ala Val  
145 150 155 160  
Glu Leu Ala Met Val Met Asp Arg Leu Tyr Gly Gly Val Cys Tyr Ala  
165 170 175  
Gly Ile Asp Thr Asp Pro Glu Leu Lys Tyr Pro Lys Gly Ala Gly Arg  
180 185 190  
Val Ala Phe Ser Asn Gln Gln Ser Tyr Ile Ala Ala Ile Ser Ala Arg  
195 200 205  
Phe Val Gln Leu Gln His Gly Glu Ile Asp Lys Arg Val Ser Leu Ile  
210 215 220  
Leu His Phe Gly Lys Phe  
225 230

SEQ ID NO:34

SEQUENCE LENGTH: 143

001000 000000

SEQUENCE TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE  
 ORGANISM: human  
 CELL TYPE: leukocyte  
 SEQUENCE DESCRIPTION: SEQ ID NO:34  
 Met Gly Ser Asp Lys Arg Val Ser Arg Thr Glu Arg Ser Gly Arg Tyr  
 1 5 10 15  
 Gly Ser Ile Ile Asp Arg Asp Asp Arg Asp Glu Arg Glu Ser Arg Ser  
 20 25 30  
 Arg Arg Arg Asp Ser Asp Tyr Lys Arg Ser Ser Asp Arg Arg Gly  
 35 40 45  
 Asp Arg Tyr Asp Asp Tyr Arg Asp Tyr Asp Ser Pro Glu Arg Glu Arg  
 50 55 60  
 Glu Arg Arg Asn Ser Asp Arg Ser Glu Asp Gly Tyr His Ser Asp Gly  
 65 70 75 80  
 Asp Tyr Gly Glu His Asp Tyr Arg His Asp Ile Ser Asp Glu Arg Glu  
 85 90 95  
 Ser Lys Thr Ile Met Leu Arg Gly Leu Pro Ile Thr Ile Thr Glu Ser  
 100 105 110  
 Asp Ile Arg Glu Met Met Glu Ser Phe Glu Gly Pro Gln Pro Ala Asp  
 115 120 125  
 Val Arg Leu Met Lys Arg Lys Thr Gly Glu Ser Leu Leu Ser Ser  
 130 135 140 143

SEQ ID NO:35  
 SEQUENCE LENGTH: 104  
 SEQUENCE TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE  
 ORGANISM: human  
 CELL TYPE: leukocyte  
 SEQUENCE DESCRIPTION: SEQ ID NO:35  
 Met Pro His Met Leu Ser Gln Leu Ile Ala Gly Gly Val Ser Thr Ser  
 1 5 10 15  
 Cys Val Thr Ala Leu Gly Glu Glu Thr Gly Ala Trp Phe Pro Val Tyr  
 20 25 30  
 Leu Ser His Ala Ser Ser Pro Phe Ala Asp Leu Val Phe Cys Pro Phe  
 35 40 45  
 Ala Glu Ile Asn His Ser Gln Glu Tyr Asp Asn Met Arg Gly Pro Val  
 50 55 60  
 Ser Pro Pro Asn Lys Gln Phe Asn Leu Gly Val Ile Phe Gly Ile Pro

65                      70                      75                      80  
 Asn Asn Cys Arg Phe Pro Thr Asp Asn Lys Ile Thr Glu Lys Gln Leu  
                             85                      90                      95  
 Leu Gly Asn Val Leu Asn Tyr Pro  
                             100

SEQ ID NO:36  
 SEQUENCE LENGTH: 133  
 SEQUENCE TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE  
 ORGANISM: human  
 CELL TYPE: leukocyte  
 SEQUENCE DESCRIPTION: SEQ ID NO:36  
 Met Asn His Pro Trp His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr  
   1                            5                            10                            15  
 Tyr Pro Thr Ala Pro Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser  
                             20                            25                            30  
 Trp Cys Arg Ser Val Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser  
                             35                            40                            45  
 Glu Asn Phe Thr Ile Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro  
                             50                            55                            60  
 Asp Gln Gly Thr Ser Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys  
   65                            70                            75                            80  
 Ser Lys Arg Glu Arg Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu  
                             85                            90                            95  
 Ser Leu Glu Pro Ala Val Ala Glu His Trp Ser Gly Glu Phe Glu Lys  
                             100                            105                            110  
 Trp Lys Val Gly Phe Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe  
                             115                            120                            125  
 Thr Arg Thr Asp Ile  
                             130

SEQ ID NO:37  
 SEQUENCE LENGTH: 133  
 SEQUENCE TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE  
 ORGANISM: human  
 CELL TYPE: leukocyte  
 SEQUENCE DESCRIPTION: SEQ ID NO:37  
 Met Asn His Pro Trp His Val Cys Phe Leu Phe Lys Val Leu Arg Tyr

1                    5                    10                    15  
 Tyr Pro Thr Ala Pro Ile Leu Lys Trp Thr His Thr Val Ser Cys Ser  
                   20                    25                    30  
 Trp Cys Arg Ser Val Leu Arg Glu Val Val Gly Asn Val Ser Leu Ser  
                   35                    40                    45  
 Glu Asn Phe Thr Ile Ser Ala Phe Cys Pro Glu Leu Thr Pro Phe Pro  
                   50                    55                    60  
 Asp Gln Gly Thr Ser Thr Met Ile Ser Phe Leu Glu Lys Phe Asn Lys  
                   65                    70                    75                    80  
 Ser Lys Arg Glu Arg Leu Glu Leu Met Leu His Phe Tyr Ser Val Leu  
                   85                    90                    95  
 Ser Leu Glu Pro Ala Phe Ala Glu His Trp Ser Gly Glu Phe Glu Lys  
                   100                    105                    110  
 Trp Lys Val Gly Phe Phe His Pro Leu Lys Arg Glu Asp Gly Phe Phe  
                   115                    120                    125  
 Thr Arg Thr Asp Ile  
                   130

SEQ ID NO:38

SEQUENCE LENGTH: 128

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE

ORGANISM: human

CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:38

Met Asp Ala Val Ala Val Tyr His Gly Lys Ile Ser Arg Glu Thr Gly  
                   1                    5                    10                    15  
 Glu Lys Leu Leu Ala Thr Gly Leu Asp Gly Ser Tyr Leu Leu Arg  
                   20                    25                    30  
 Asp Ser Glu Ser Val Pro Gly Val Tyr Cys Leu Cys Val Leu Tyr His  
                   35                    40                    45  
 Gly Tyr Ile Tyr Thr Tyr Arg Val Ser Gln Thr Glu Thr Gly Ser Trp  
                   50                    55                    60  
 Ser Ala Glu Thr Ala Pro Gly Val His Lys Arg Tyr Phe Arg Lys Ile  
                   65                    70                    75                    80  
 Lys Asn Leu Ile Ser Ala Phe Gln Lys Pro Asp Gln Gly Ile Val Ile  
                   85                    90                    95  
 Pro Leu Gln Tyr Pro Val Glu Lys Lys Ser Ser Ala Arg Ser Thr Gln  
                   100                    105                    110  
 Gly Thr Thr Gly Ile Arg Glu Asp Pro Asp Val Cys Leu Lys Ala Pro  
                   115                    120                    125





AATTCCTCC CCACTGGGG AAAGCAAATC ATCAGGCCCA TTGCAAAAC TGCTCTTGGT 120  
TGAGCTTCT GCCTTAAATC ATACCCACAG TGAATGGCGT CCCTTTATCA CCGCTAATGA 180  
CTCTGACATC TCTCTCACT CACATGTGAG CCTCCTCAGC TCTCGANAAA CAAGTCNGTC 240  
TCGG 244

SEQ ID NO:42  
SEQUENCE LENGTH: 258  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE  
ORGANISM: human  
CELL TYPE: leukocyte

SEQUENCE DESCRIPTION: SEQ ID NO:42  
TCTCAGAAAA CTCCAGATCA AATGAGATGA GTATGGTGNV NAGGGCTGGC AATTAGAGGA 60  
TACTCTCAA TGGTGATGAA GGGAGATGTC TGGGGGAAAT CCAGCAGGAT GTTGATTAG 120  
TATGTACACA GTGAGAGGAT ACTTGAGAG AACCTAGAAT CTTCTCTGAA TGTGACGGGC 180  
CCTCAGAGAT AATTGTTAAC AGATAAGTGG ATGATTAAAT ACACCTCCTC CAGTAGGCTA 240  
GATGTTAAGA CGGAGATC 258

SEQ ID NO:43  
SEQUENCE LENGTH: 26  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:43  
GGGCTTAATA TTATTCATAG ATCGAG 26

SEQ ID NO:44  
SEQUENCE LENGTH: 26  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:44  
GTTATTATAC TATCAAGTAA CCCAAC 26

SEQ ID NO:45  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:45  
GTGGATCTGG ATTTTGTCA TATGT

SEQ ID NO:46  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:46  
GTTTGTGATT ATAACCAAC ATGTG

SEQ ID NO:47  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:47  
GAAGGGGAAG AGACATTAA TTATC

SEQ ID NO:48  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:48  
GCTTCTAAAT CTCCTGAGTC ACTT

SEQ ID NO:49  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:49  
GACAATGAGT AAGAAGAAAG AGGG

SEQ ID NO:50  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single





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SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:60  
GCCAACATCT GAACTAAATA CTGC 24

SEQ ID NO:61  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:61  
GTTTCAGTGAA TGTTACCTAG AAACA 25

SEQ ID NO:62  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:62  
GGAGTGAAAA CTGTCTTGTT CATC 24

SEQ ID NO:63  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:63  
GTATGACAAA TAGTTTCTGC CTGAT 25

SEQ ID NO:64  
SEQUENCE LENGTH: 25  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:64  
GATTAACAAA GATGTACAGA CTGAG 25

SEQ ID NO:65

SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:65  
GAGACAGCAT TCAGATATAG ACGG

```

SEQ ID NO:66
SEQUENCE LENGTH: 22
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
SEQUENCE DESCRIPTION: SEQ ID NO:66
CGGTGGAATC AAATGGACTG GC

```

SEQ ID NO:67  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:67  
GATGGCCTGT GTGAACAGAT TAAT

```

SEQ ID NO:68
SEQUENCE LENGTH: 24
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
SEQUENCE DESCRIPTION: SEQ ID NO:68
GAGAGAGATG TCAGAGTCAT TAGC

```

SEQ ID NO:69  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:69  
GATCCCCACA ATTTCITGTG ATTG 24







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- 102 -

**Abstract** The purpose of this study was to determine the effect of a 12-week training program on the physical fitness of 10-year-old children. The study was conducted in a primary school in the city of Ankara, Turkey. The study group consisted of 20 children (10 boys and 10 girls) who were randomly selected from the 10-year-old children in the school. The children were divided into two groups: a control group and an experimental group. The control group did not participate in any physical education program, while the experimental group participated in a 12-week training program. The physical fitness of the children was measured at the beginning and at the end of the 12-week period. The measurements included maximum heart rate, maximum oxygen consumption, maximum power, and maximum speed. The results of the study showed that the experimental group had significantly higher values for all four measurements at the end of the 12-week period compared to the control group. The results suggest that a 12-week training program can improve the physical fitness of 10-year-old children.

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- 103 -

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- 104 -

TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid, synthetic DNA  
 SEQUENCE DESCRIPTION: SEQ ID NO:94  
 GTCTTCAGGA AAATTGTAGT TACAG

```

SEQ ID NO:95
SEQUENCE LENGTH: 24
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
SEQUENCE DESCRIPTION: SEQ ID NO:95
GTTACAAACA CACACGAAGT TCCT

```

```

SEQ ID NO:96
SEQUENCE LENGTH: 22
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
SEQUENCE DESCRIPTION: SEQ ID NO:96
GACTTCCTAA GGCACACTCA GC

```

```

SEQ ID NO:97
SEQUENCE LENGTH: 24
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
SEQUENCE DESCRIPTION: SEQ ID NO:97
GTTTAACTAC CTCACGGTC ATGA

```

```

SEQ ID NO:98
SEQUENCE LENGTH: 22
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
SEQUENCE DESCRIPTION: SEQ ID NO:98
GTCGCCAAGG CTGTACTGCA AT

```

SEQ ID NO:99  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid

Seq ID: 99-104

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:99  
GAAATAGGTA TCCCTTGATG TCGA 24

SEQ ID NO:100  
SEQUENCE LENGTH: 24  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:100  
GACCAAGAAT TCAGTTCATC AGTT 24

SEQ ID NO:101  
SEQUENCE LENGTH: 22  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:101  
GAATGAACCA GAGCCAGGAC AG 22

SEQ ID NO:102  
SEQUENCE LENGTH: 22  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:102  
GCCTTGATG TATCCCTGTG CC 22

SEQ ID NO:103  
SEQUENCE LENGTH: 21  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:103  
AAGAGTCCAC CAGGCCATGG A 21

SEQ ID NO:104  
SEQUENCE LENGTH: 23

Seq ID "104" "105" "106" "107" "108" "109"

SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:104  
TACCTTGTGT ACTTCTAGCT GAG 23

SEQ ID NO:105  
SEQUENCE LENGTH: 17  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:105  
GTTTTTTTTT TTTTITA 17

SEQ ID NO:106  
SEQUENCE LENGTH: 17  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:106  
GTTTTTTTTT TTTTITG 17

SEQ ID NO:107  
SEQUENCE LENGTH: 17  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:107  
GTTTTTTTTT TTTTITC 17

SEQ ID NO:108  
SEQUENCE LENGTH: 18  
SEQUENCE TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid, synthetic DNA  
SEQUENCE DESCRIPTION: SEQ ID NO:108  
CAGAGTGATG GATATCAA 18

SEQ ID NO:109

```
SEQUENCE LENGTH: 22
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
SEQUENCE DESCRIPTION: SEQ ID NO:109
ATGAAAGTGC CAGTGTCCCA TG
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SEQ ID NO:110
SEQUENCE LENGTH: 22
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
SEQUENCE DESCRIPTION: SEQ ID NO:110
CCCATCACCA TCTCCAGGA GC

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SEQ ID NO:111
SEQUENCE LENGTH: 26
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
SEQUENCE DESCRIPTION: SEQ ID NO:111
TTCACCACT TCTGATGTC ATCATA

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